



1600

RAW SEQUENCE LISTING

DATE: 02/03/2003

PATENT APPLICATION: US/09/875,321A

TIME: 09:15:39

Input Set : A:\Sequence listing.TXT

Output Set: N:\CRF4\02032003\I875321A.raw

4 <110> APPLICANT: Curtis, Rory A.J.
6 <120> TITLE OF INVENTION: 52906, 33408, AND 12189, NOVEL POTASSIUM
7 CHANNEL FAMILY MEMBERS AND USES THEREOF
10 <130> FILE REFERENCE: 10448-061001
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/875,321A
C--> 12 <141> CURRENT FILING DATE: 2000-06-06
12 <150> PRIOR APPLICATION NUMBER: US 60/209,845
13 <151> PRIOR FILING DATE: 2000-06-06
15 <160> NUMBER OF SEQ ID NOS: 13
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 3525
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (638)...(3178)
28 <400> SEQUENCE: 1

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30	tcccgcagcg gccaaaggcag ggctcaggcc ccgggattct ccccacacgc tgctgcaactg	120
31	gcgcagcccg tcgccaaact ttttctcccc aaagccagtg ccccgagct tacttgccgg	180
32	gcagccggca gccactctc ggccgggatga tctgggagaa gcgggctgg gacgaggggg	240
33	ctgctgtttt gcagccctgc gaggcgtgca gtcggagaag tggctcgggg tccacaccgt	300
34	ccctgagcct gcccctggc caaggtggcc cgacgtgctg cagtggctgg cgcaggtgat	360
35	ccgggcagcg cgtccggcac tagtcaagg ggagcggca cgggaggag gggcgcttt	420
36	ctcttttctc ctcccctgc agcccagctg cactgcgtgg gggtctcca tctccacgca	480
37	atcagcaggc ggaatccctg ccctggagcg ccctggctct ggactgcacc cccctagggt	540
38	ttgtcctgca gattctctc cccatcttc tctgccacac acgcttccct aagccgcgcg	600
39	cgccgcaaac tcagtcctcg tccccgcagg tgatgtc atg ccc att gtt ttg gtg	655
40	Met Pro Ile Val Leu Val	
41	1 5	
43	cgc cca acc aat cgg act cgc cgc ctg gat tct acc gga gcc ggc atg	703
44	Arg Pro Thr Asn Arg Thr Arg Arg Leu Asp Ser Thr Gly Ala Gly Met	
45	10 15 20	
47	ggc cct tcc tcg cac cag cag cag gag tcc ccg ctc ccg acc ata acg	751
48	Gly Pro Ser Ser His Gln Gln Gln Glu Ser Pro Leu Pro Thr Ile Thr	
49	25 30 35	
51	cat tgc gca ggg tgc acc acc gct tgg tct ccc tgc agc ttt aac agc	799
52	His Cys Ala Gly Cys Thr Thr Ala Trp Ser Pro Cys Ser Phe Asn Ser	
53	40 45 50	
55	cct gac atg gaa acc cca ttg cag ttc cag cgc ggc ttc ttc cca gag	847
56	Pro Asp Met Glu Thr Pro Leu Gln Phe Gln Arg Gly Phe Phe Pro Glu	
57	55 60 65 70	

ENTERED

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59	cag ccg ccg ccg ccg ccg ccg tcc tca cac ctg cat tgc cag cag cag	895
60	Gln Pro Pro Pro Pro Pro Arg Ser Ser His Leu His Cys Gln Gln Gln	
61	75 80 85	
63	caa cag agc cag gac aag ccg tgc ccg ccc ttc gcg ccc ctc ccg cac	943
64	Gln Gln Ser Gln Asp Lys Pro Cys Pro Pro Phe Ala Pro Leu Pro His	
65	90 95 100	
67	cct cac cac cac ccg cac ctc gcg cac cag cag ccg gcc agc ggc ggc	991
68	Pro His His His Pro His Leu Ala His Gln Gln Pro Ala Ser Gly Gly	
69	105 110 115	
71	agc agc cca tgc ctc ccg tgc aac agc tgc gcc tcc tcc ggt gcc ccg	1039
72	Ser Ser Pro Cys Leu Arg Cys Asn Ser Cys Ala Ser Ser Gly Ala Pro	
73	120 125 130	
75	gcg gcg ggg gcg gga gat aac ctg tcc ctg ctg ctc cgc acc tcc tcg	1087
76	Ala Ala Gly Ala Gly Asp Asn Leu Ser Leu Leu Leu Arg Thr Ser Ser	
77	135 140 145 150	
79	ccc ggc ggc gcc ttc ccg acc cgc acc tcc tcg ccg ctg tcg ggc tcg	1135
80	Pro Gly Gly Ala Phe Arg Thr Arg Thr Ser Ser Pro Leu Ser Gly Ser	
81	155 160 165	
83	tcc tgc tgc tgc tgc tgc tgc tcg tcg cgc ccg ggc agc cag ctc aat	1183
84	Ser Cys Cys Cys Cys Cys Cys Ser Ser Arg Arg Gly Ser Gln Leu Asn	
85	170 175 180	
87	gtg agc gag ctg acg ccg tcc agc cat gcc agt gcg ctc ccg cag cag	1231
88	Val Ser Glu Leu Thr Pro Ser Ser His Ala Ser Ala Leu Arg Gln Gln	
89	185 190 195	
91	tac gcg cag cag tcc gcg cag cag tcg gcg tcc gcc tcc cag tac cac	1279
92	Tyr Ala Gln Gln Ser Ala Gln Gln Ser Ala Ser Ala Ser Gln Tyr His	
93	200 205 210	
95	cag tgc cac agc ctg cag ccc gcc gcc agc ccc acg ggc agc ctc ggc	1327
96	Gln Cys His Ser Leu Gln Pro Ala Ala Ser Pro Thr Gly Ser Leu Gly	
97	215 220 225 230	
99	agt ctg ggc tcc ggg ccc ccg ctc tcg cac cac cac cac cac ccg cac	1375
100	Ser Leu Gly Ser Gly Pro Pro Leu Ser His His His His His Pro His	
101	235 240 245	
103	ccg gcg cac cac cag cac cac cag ccc cag gcg cgc cgc gag agc aac	1423
104	Pro Ala His His Gln His His Gln Pro Gln Ala Arg Arg Glu Ser Asn	
105	250 255 260	
107	ccc ttc acc gaa ata gcc atg agc agc tgc agg tac aac ggg ggc gtc	1471
108	Pro Phe Thr Glu Ile Ala Met Ser Ser Cys Arg Tyr Asn Gly Gly Val	
109	265 270 275	
111	atg ccg ccg ctc agc aac ttg agc gcg tcc cgc ccg aac ctg cac gag	1519
112	Met Arg Pro Leu Ser Asn Leu Ser Ala Ser Arg Arg Asn Leu His Glu	
113	280 285 290	
115	atg gac tca gag gcg cag ccc ctg cag ccc ccc gcg tct gtc gga gga	1567
116	Met Asp Ser Glu Ala Gln Pro Leu Gln Pro Pro Ala Ser Val Gly Gly	
117	295 300 305 310	
119	ggt ggc ggc gcg tcc tcc ccg tct gca gcc gct gcc gcc gcc gcc gct	1615
120	Gly Gly Gly Ala Ser Ser Pro Ser Ala Ala Ala Ala Ala Ala Ala Ala	
121	315 320 325	
123	gtt tcg tcc tca gcc ccc gag atc gtg gtg tct aag ccc gag cac aac	1663

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124	Val	Ser	Ser	Ser	Ala	Pro	Glu	Ile	Val	Val	Ser	Lys	Pro	Glu	His	Asn	
125				330					335					340			
127	aac	tcc	aac	aac	ctg	gcg	ctc	tat	gga	acc	ggc	ggc	gga	ggc	agc	act	1711
128	Asn	Ser	Asn	Asn	Leu	Ala	Leu	Tyr	Gly	Thr	Gly	Gly	Gly	Gly	Ser	Thr	
129			345					350						355			
131	gga	gga	ggc	ggc	ggc	ggt	ggc	ggg	agc	ggg	cac	ggc	agc	agc	agt	ggc	1759
132	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Ser	Gly	His	Gly	Ser	Ser	Ser	Gly	
133		360						365						370			
135	acc	aag	tcc	agc	aaa	aag	aaa	aac	cag	aac	atc	ggc	tac	aag	ctg	ggc	1807
136	Thr	Lys	Ser	Ser	Lys	Lys	Lys	Asn	Gln	Asn	Ile	Gly	Tyr	Lys	Leu	Gly	
137	375					380					385					390	
139	cac	cgg	cgc	gcc	ctg	ttc	gaa	aag	cgc	aag	cgg	ctc	agc	gac	tac	gcg	1855
140	His	Arg	Arg	Ala	Leu	Phe	Glu	Lys	Arg	Lys	Arg	Leu	Ser	Asp	Tyr	Ala	
141				395						400					405		
143	ctc	atc	ttc	ggc	atg	ttc	ggc	atc	gtg	gtc	atg	gtc	atc	gag	acc	gag	1903
144	Leu	Ile	Phe	Gly	Met	Phe	Gly	Ile	Val	Val	Met	Val	Ile	Glu	Thr	Glu	
145			410					415						420			
147	ctg	tcg	tgg	ggc	gcc	tac	gac	aag	gcg	tcg	ctg	tat	tcc	tta	gct	ctg	1951
148	Leu	Ser	Trp	Gly	Ala	Tyr	Asp	Lys	Ala	Ser	Leu	Tyr	Ser	Leu	Ala	Leu	
149			425					430						435			
151	aaa	tgc	ctt	atc	agt	ctc	tcc	acg	atc	atc	ctg	ctc	ggt	ctg	atc	atc	1999
152	Lys	Cys	Leu	Ile	Ser	Leu	Ser	Thr	Ile	Ile	Leu	Leu	Gly	Leu	Ile	Ile	
153		440						445					450				
155	gtg	tac	cac	gcc	agg	gaa	ata	cag	ttg	ttc	atg	gtg	gac	aat	gga	gca	2047
156	Val	Tyr	His	Ala	Arg	Glu	Ile	Gln	Leu	Phe	Met	Val	Asp	Asn	Gly	Ala	
157	455					460				465					470		
159	gat	gac	tgg	aga	ata	gcc	atg	act	tat	gag	cgt	att	ttc	ttc	atc	tgc	2095
160	Asp	Asp	Trp	Arg	Ile	Ala	Met	Thr	Tyr	Glu	Arg	Ile	Phe	Phe	Ile	Cys	
161				475					480						485		
163	ttg	gaa	ata	ctg	gtg	tgt	gct	att	cat	ccc	ata	cct	ggg	aat	tat	aca	2143
164	Leu	Glu	Ile	Leu	Val	Cys	Ala	Ile	His	Pro	Ile	Pro	Gly	Asn	Tyr	Thr	
165			490					495						500			
167	ttc	aca	tgg	acg	gcc	cgg	ctt	gcc	ttc	tcc	tat	gcc	cca	tcc	aca	acc	2191
168	Phe	Thr	Trp	Thr	Ala	Arg	Leu	Ala	Phe	Ser	Tyr	Ala	Pro	Ser	Thr	Thr	
169			505					510						515			
171	acc	gct	gat	gtg	gat	att	att	tta	tct	ata	cca	atg	ttc	tta	aga	ctc	2239
172	Thr	Ala	Asp	Val	Asp	Ile	Ile	Leu	Ser	Ile	Pro	Met	Phe	Leu	Arg	Leu	
173		520						525					530				
175	tat	ctg	att	gcc	aga	gtc	atg	ctt	tta	cat	agc	aaa	ctt	ttc	act	gat	2287
176	Tyr	Leu	Ile	Ala	Arg	Val	Met	Leu	Leu	His	Ser	Lys	Leu	Phe	Thr	Asp	
177	535					540					545				550		
179	acc	tcc	tct	aga	agc	att	gga	gca	ctt	aat	aag	ata	aac	ttc	aat	aca	2335
180	Thr	Ser	Ser	Arg	Ser	Ile	Gly	Ala	Leu	Asn	Lys	Ile	Asn	Phe	Asn	Thr	
181				555						560					565		
183	cgt	ttt	gtt	atg	aag	act	tta	atg	act	ata	tgc	cca	gga	act	gta	ctc	2383
184	Arg	Phe	Val	Met	Lys	Thr	Leu	Met	Thr	Ile	Cys	Pro	Gly	Thr	Val	Leu	
185			570					575						580			
187	ttg	gtt	ttt	agt	atc	tca	tta	tgg	ata	att	gcc	gca	tgg	act	gtc	cga	2431
188	Leu	Val	Phe	Ser	Ile	Ser	Leu	Trp	Ile	Ile	Ala	Ala	Trp	Thr	Val	Arg	

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189	585	590	595	
191	gct tgt gaa agg tac cat gat caa cag gat gtt act agc aac ttc ctt	2479		
192	Ala Cys Glu Arg Tyr His Asp Gln Gln Asp Val Thr Ser Asn Phe Leu			
193	600 605 610			
195	gga gcg atg tgg ttg ata tca ata act ttt ctc tcc att ggt tat ggt	2527		
196	Gly Ala Met Trp Leu Ile Ser Ile Thr Phe Leu Ser Ile Gly Tyr Gly			
197	615 620 625 630			
199	gac atg gta cct aac aca tac tgt gga aaa gga gtc tgc tta ctt act	2575		
200	Asp Met Val Pro Asn Thr Tyr Cys Gly Lys Gly Val Cys Leu Leu Thr			
201	635 640 645			
203	gga att atg ggt gct ggt tgc aca gcc ctg gtg gta gct gta gtg gca	2623		
204	Gly Ile Met Gly Ala Gly Cys Thr Ala Leu Val Val Ala Val Val Ala			
205	650 655 660			
207	agg aag cta gaa ctt acc aaa gca gaa aaa cac gtg cac aat ttc atg	2671		
208	Arg Lys Leu Glu Leu Thr Lys Ala Glu Lys His Val His Asn Phe Met			
209	665 670 675			
211	atg gat act cag ctg act aaa aga gta aaa aat gca gct gcc aat gta	2719		
212	Met Asp Thr Gln Leu Thr Lys Arg Val Lys Asn Ala Ala Ala Asn Val			
213	680 685 690			
215	ctc agg gaa aca tgg cta att tac aaa aat aca aag cta gtg aaa aag	2767		
216	Leu Arg Glu Thr Trp Leu Ile Tyr Lys Asn Thr Lys Leu Val Lys Lys			
217	695 700 705 710			
219	ata gat cat gca aaa gta aga aaa cat caa cga aaa ttc ctg caa gct	2815		
220	Ile Asp His Ala Lys Val Arg Lys His Gln Arg Lys Phe Leu Gln Ala			
221	715 720 725			
223	att cat caa tta aga agt gta aaa atg gag cag agg aaa ctg aat gac	2863		
224	Ile His Gln Leu Arg Ser Val Lys Met Glu Gln Arg Lys Leu Asn Asp			
225	730 735 740			
227	caa gca aac act ttg gtg gac ttg gca aag acc cag aac atc atg tat	2911		
228	Gln Ala Asn Thr Leu Val Asp Leu Ala Lys Thr Gln Asn Ile Met Tyr			
229	745 750 755			
231	gat atg att tct gac tta aac gaa agg agt gaa gac ttc gag aag agg	2959		
232	Asp Met Ile Ser Asp Leu Asn Glu Arg Ser Glu Asp Phe Glu Lys Arg			
233	760 765 770			
235	att gtt acc ctg gaa aca aaa cta gag act ttg att ggt agc atc cac	3007		
236	Ile Val Thr Leu Glu Thr Lys Leu Glu Thr Leu Ile Gly Ser Ile His			
237	775 780 785 790			
239	gcc ctc cct ggg ctc ata agc cag acc atc agg cag cag cag aga gat	3055		
240	Ala Leu Pro Gly Leu Ile Ser Gln Thr Ile Arg Gln Gln Gln Arg Asp			
241	795 800 805			
243	ttc att gag gct cag atg gag agc tac gac aag cac gtc act tac aat	3103		
244	Phe Ile Glu Ala Gln Met Glu Ser Tyr Asp Lys His Val Thr Tyr Asn			
245	810 815 820			
247	gct gag cgg tcc cgg tcc tcg tcc agg agg cgg cgg tcc tct tcc aca	3151		
248	Ala Glu Arg Ser Arg Ser Ser Ser Arg Arg Arg Arg Ser Ser Ser Thr			
249	825 830 835			
251	gca cca cca act tca tca gag agt agc tagaagagaa taagttaacc	3198		
252	Ala Pro Pro Thr Ser Ser Glu Ser Ser			
253	840 845			

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255 acaaaataag actttttgcc atcatatggt caatatttta gctttttattg taaagcccct 3258
256 atggttctaa tcagcgttat ccgggttctg atgtcagaat cctgggaacc tgaacactaa 3318
257 gtttttaggcc aaaatgagtg aaaactcttt ttttttcttt cagatgcaca gggaatgcac 3378
258 ctattattgc tatatagatt gttcctcctg taatttcact aactttttat tcatgcactt 3438
259 caaacaact ttactactac attatatgat atataataaa aaaagttaat ttctgcaaaa 3498
260 aaaaaaaaaa aaaaaaaaaa ggacggg 3525
262 <210> SEQ ID NO: 2
263 <211> LENGTH: 847
264 <212> TYPE: PRT
265 <213> ORGANISM: Homo sapiens
267 <400> SEQUENCE: 2
268 Met Pro Ile Val Leu Val Arg Pro Thr Asn Arg Thr Arg Arg Leu Asp
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270 Ser Thr Gly Ala Gly Met Gly Pro Ser Ser His Gln Gln Gln Glu Ser
271 20 25 30
272 Pro Leu Pro Thr Ile Thr His Cys Ala Gly Cys Thr Thr Ala Trp Ser
273 35 40 45
274 Pro Cys Ser Phe Asn Ser Pro Asp Met Glu Thr Pro Leu Gln Phe Gln
275 50 55 60
276 Arg Gly Phe Phe Pro Glu Gln Pro Pro Pro Pro Pro Arg Ser Ser His
277 65 70 75 80
278 Leu His Cys Gln Gln Gln Gln Ser Gln Asp Lys Pro Cys Pro Pro
279 85 90 95
280 Phe Ala Pro Leu Pro His Pro His His Pro His Leu Ala His Gln
281 100 105 110
282 Gln Pro Ala Ser Gly Gly Ser Ser Pro Cys Leu Arg Cys Asn Ser Cys
283 115 120 125
284 Ala Ser Ser Gly Ala Pro Ala Ala Gly Ala Gly Asp Asn Leu Ser Leu
285 130 135 140
286 Leu Leu Arg Thr Ser Ser Pro Gly Gly Ala Phe Arg Thr Arg Thr Ser
287 145 150 155 160
288 Ser Pro Leu Ser Gly Ser Ser Cys Cys Cys Cys Cys Cys Ser Ser Arg
289 165 170 175
290 Arg Gly Ser Gln Leu Asn Val Ser Glu Leu Thr Pro Ser Ser His Ala
291 180 185 190
292 Ser Ala Leu Arg Gln Gln Tyr Ala Gln Gln Ser Ala Gln Gln Ser Ala
293 195 200 205
294 Ser Ala Ser Gln Tyr His Gln Cys His Ser Leu Gln Pro Ala Ala Ser
295 210 215 220
296 Pro Thr Gly Ser Leu Gly Ser Leu Gly Ser Gly Pro Pro Leu Ser His
297 225 230 235 240
298 His His His His Pro His Pro Ala His His Gln His His Gln Pro Gln
299 245 250 255
300 Ala Arg Arg Glu Ser Asn Pro Phe Thr Glu Ile Ala Met Ser Ser Cys
301 260 265 270
302 Arg Tyr Asn Gly Gly Val Met Arg Pro Leu Ser Asn Leu Ser Ala Ser
303 275 280 285
304 Arg Arg Asn Leu His Glu Met Asp Ser Glu Ala Gln Pro Leu Gln Pro
305 290 295 300

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VERIFICATION SUMMARY

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Output Set: N:\CRF4\02032003\I875321A.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date